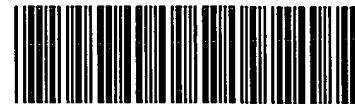


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**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/690,276A
Source: FW/6
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DATE: 09/18/2006

PATENT APPLICATION: US/10/690,276A

TIME: 15:02:07

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3 <110> APPLICANT: Myriad Genetics, Incorporated
4 Cimborra, Daniel
5 Heichman, Karen
6 Bartel, Paul
7 Mauck, Kimberly
8 Bush, Angie
10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
12 <130> FILE REFERENCE: 1834.01
14 <140> CURRENT APPLICATION NUMBER: US 10/690,276A
15 <141> CURRENT FILING DATE: 2003-10-20
17 <150> PRIOR APPLICATION NUMBER: 09/727,384
18 <151> PRIOR FILING DATE: 2000-12-01
20 <150> PRIOR APPLICATION NUMBER: 60/168,377
21 <151> PRIOR FILING DATE: 1999-12-02
23 <150> PRIOR APPLICATION NUMBER: 60/168,379
24 <151> PRIOR FILING DATE: 1999-12-02
26 <150> PRIOR APPLICATION NUMBER: 60/185,056
27 <151> PRIOR FILING DATE: 2000-02-25
29 <150> PRIOR APPLICATION NUMBER: 10/035,344
30 <151> PRIOR FILING DATE: 2002-01-04
32 <150> PRIOR APPLICATION NUMBER: 60/259,571
33 <151> PRIOR FILING DATE: 2001-01-04
35 <150> PRIOR APPLICATION NUMBER: 10/035,343
36 <151> PRIOR FILING DATE: 2002-01-04
38 <150> PRIOR APPLICATION NUMBER: 60/259,572
39 <151> PRIOR FILING DATE: 2001-01-04
41 <150> PRIOR APPLICATION NUMBER: 10/099,924
42 <151> PRIOR FILING DATE: 2002-03-14
44 <150> PRIOR APPLICATION NUMBER: 60/276,179
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50 <150> PRIOR APPLICATION NUMBER: 60/343,818
51 <151> PRIOR FILING DATE: 2001-10-25
53 <150> PRIOR APPLICATION NUMBER: 10/100,503
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57 <151> PRIOR FILING DATE: 2001-03-19
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63 <151> PRIOR FILING DATE: 2000-12-14
65 <150> PRIOR APPLICATION NUMBER: 10/024,599

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68 <150> PRIOR APPLICATION NUMBER: 60/256,986
69 <151> PRIOR FILING DATE: 2000-12-21
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77 <212> TYPE: DNA
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89          Met Val Ala Asn Phe Phe Lys Ser Leu Ile Leu Pro
90          1          5          10
92 tac att cat aag ctt tgc aaa gga atg ttt aca aag aaa ttg gga aat      160
93 Tyr Ile His Lys Leu Cys Lys Gly Met Phe Thr Lys Lys Leu Gly Asn
94          15          20          25
96 aca aac aaa aac aaa gag tat cgt cag cag aaa aag gat caa gac ttc      208
97 Thr Asn Lys Asn Lys Glu Tyr Arg Gln Gln Lys Lys Asp Gln Asp Phe
98          30          35          40
100 ccc act gct ggc cag acc aaa tcc ccc aaa ttt tct tac act ttt aaa      256
101 Pro Thr Ala Gly Gln Thr Lys Ser Pro Lys Phe Ser Tyr Thr Phe Lys
102 45          50          55          60
104 agc act gta aag aag att gca aag tgt tca tcc act cac aac tta tcc      304
105 Ser Thr Val Lys Lys Ile Ala Lys Cys Ser Ser Thr His Asn Leu Ser
106          65          70          75
108 act gag gaa gac gag gcc agt aaa gag ttt tcc ctc tca cca aca ttc      352
109 Thr Glu Glu Asp Glu Ala Ser Lys Glu Phe Ser Leu Ser Pro Thr Phe
110          80          85          90
112 agt tac cga gta gct att gcc aat ggc cta caa aag aat gct aaa gta      400
113 Ser Tyr Arg Val Ala Ile Ala Asn Gly Leu Gln Lys Asn Ala Lys Val
114          95          100          105
116 acc acc agt gat aat gag gat ctg ctt caa gag ctc tct tca atc gag      448
117 Thr Thr Ser Asp Asn Glu Asp Leu Leu Gln Glu Leu Ser Ser Ile Glu
118          110          115          120
120 agt tcc tac tca gaa tca tta aat gaa cta agg agt agc aca gaa aac      496
121 Ser Ser Tyr Ser Glu Ser Leu Asn Glu Leu Arg Ser Ser Thr Glu Asn
122 125          130          135          140
124 cag gca caa tca aca cac aca atg cca gtt aga cgc aac aga aag agt      544
125 Gln Ala Gln Ser Thr His Thr Met Pro Val Arg Arg Asn Arg Lys Ser
126          145          150          155
128 tca agc agc ctt gca ccc tct gag ggc agc tct gac ggg gag cgt act      592
129 Ser Ser Ser Leu Ala Pro Ser Glu Gly Ser Ser Asp Gly Glu Arg Thr
130          160          165          170
132 cta cat ggc tta aaa ctg gga gct tta cga aaa ctg aga aaa tgg aaa      640
133 Leu His Gly Leu Lys Leu Gly Ala Leu Arg Lys Leu Arg Lys Trp Lys

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138	190	195	200	
140	aaa tcc tgg gga ata aga agt aag tct ttg gac aga act gtc cga aac	736		
141	Lys Ser Trp Gly Ile Arg Ser Lys Ser Leu Asp Arg Thr Val Arg Asn			
142	205	210	215	220
144	cca aag aca aat gcc ctg gag cca ggg ttc agt tcc tct ggc tgc att	784		
145	Pro Lys Thr Asn Ala Leu Glu Pro Gly Phe Ser Ser Ser Gly Cys Ile			
146	225	230	235	
148	agc caa aca cat gat gtc atg gaa atg atc ttt aag gaa ctt cag gga	832		
149	Ser Gln Thr His Asp Val Met Glu Met Ile Phe Lys Glu Leu Gln Gly			
150	240	245	250	
152	ata agt cag att gaa aca gaa ctt tct gaa cta cga ggg cac gtc aat	880		
153	Ile Ser Gln Ile Glu Thr Glu Leu Ser Glu Leu Arg Gly His Val Asn			
154	255	260	265	
156	gct ctc aag cac tcc atc gat gag atc tcc agc agt gtg gag gtt gta	928		
157	Ala Leu Lys His Ser Ile Asp Glu Ile Ser Ser Ser Val Glu Val Val			
158	270	275	280	
160	caa agt gaa att gag cag ttg cgc aca ggg ttt gtc cag tct cgg agg	976		
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164	gaa act aga gac atc cat gat tat att aag cac tta ggt cat atg ggt	1024		
165	Glu Thr Arg Asp Ile His Asp Tyr Ile Lys His Leu Gly His Met Gly			
166	305	310	315	
168	agc aag gca agc ctg aga ttt tta aat gtg act gaa gaa aga ttt gaa	1072		
169	Ser Lys Ala Ser Leu Arg Phe Leu Asn Val Thr Glu Glu Arg Phe Glu			
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172	tat gtt gaa agc gtg gtg tac caa att cta ata gat aaa atg ggt ttt	1120		
173	Tyr Val Glu Ser Val Val Tyr Gln Ile Leu Ile Asp Lys Met Gly Phe			
174	335	340	345	
176	tca gat gca cca aat gct att aaa att gaa ttt gct cag agg ata gga	1168		
177	Ser Asp Ala Pro Asn Ala Ile Lys Ile Glu Phe Ala Gln Arg Ile Gly			
178	350	355	360	
180	cac cag aga gac tgc cca aat gca aag cct cga ccc ata ctt gtg tac	1216		
181	His Gln Arg Asp Cys Pro Asn Ala Lys Pro Arg Pro Ile Leu Val Tyr			
182	365	370	375	380
184	ttt gaa acc cct caa caa agg gat tct gtc tta aaa aag tca tat aaa	1264		
185	Phe Glu Thr Pro Gln Gln Arg Asp Ser Val Leu Lys Lys Ser Tyr Lys			
186	385	390	395	
188	ctc aaa gga aca ggc att gga atc tca aca gat att cta act cat gac	1312		
189	Leu Lys Gly Thr Gly Ile Gly Ile Ser Thr Asp Ile Leu Thr His Asp			
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192	atc aga gaa aga aaa gag aaa ggg ata cca tcc tcc cag aca tat gag	1360		
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196	agc atg gct ata aag ttg tct act cca gag cca aaa atc aag aag aac	1408		
197	Ser Met Ala Ile Lys Leu Ser Thr Pro Glu Pro Lys Ile Lys Lys Asn			
198	430	435	440	

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202	445					450				455						460	
204	aat	aga	aac	agt	tac	gct	gtg	ctt	tcc	aag	tca	gag	ctt	cta	aca	aag	1504
205	Asn	Arg	Asn	Ser	Tyr	Ala	Val	Leu	Ser	Lys	Ser	Glu	Leu	Leu	Thr	Lys	
206					465					470						475	
208	gga	agt	act	tcc	aaq	cca	aqc	tca	aaa	tca	cac	agt	gct	aga	tcc	aag	1552
209	Gly	Ser	Thr	Ser	Lys	Pro	Ser	Ser	Lys	Ser	His	Ser	Ala	Arg	Ser	Lys	
210				480					485					490			
212	aat	aaa	act	gct	aat	agc	agc	aga	att	tca	aat	aaa	tca	gat	tat	gat	1600
213	Asn	Lys	Thr	Ala	Asn	Ser	Ser	Arg	Ile	Ser	Asn	Lys	Ser	Asp	Tyr	Asp	
214			495					500					505				
216	aaa	atc	tcc	tca	cag	ttg	cca	gaa	tca	gat	atc	ttg	gaa	aag	caa	acc	1648
217	Lys	Ile	Ser	Ser	Gln	Leu	Pro	Glu	Ser	Asp	Ile	Leu	Glu	Lys	Gln	Thr	
218		510					515					520					
220	aca	acc	cat	tat	gca	gat	gca	aca	cct	ctc	tgg	cac	tca	cag	agt	gat	1696
221	Thr	Thr	His	Tyr	Ala	Asp	Ala	Thr	Pro	Leu	Trp	His	Ser	Gln	Ser	Asp	
222	525				530					535						540	
224	ttt	ttc	act	gct	aaa	ttt	agt	cgt	tct	gaa	tca	gat	ttt	tcc	aaa	ttg	1740
225	Phe	Phe	Thr	Ala	Lys	Leu	Ser	Arg	Ser	Glu	Ser	Asp	Phe	Ser	Lys	Leu	
226					545					550					555		
228	tgt	cag	tct	tac	tca	gaa	gat	ttt	tca	gaa	aat	cag	ttt	ttc	act	aga	1792
229	Cys	Gln	Ser	Tyr	Ser	Glu	Asp	Phe	Ser	Glu	Asn	Gln	Phe	Phe	Thr	Arg	
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232	act	aat	gga	agc	tct	ctc	ctg	tca	tct	tcg	gac	cgg	gag	cta	tgg	cag	1840
233	Thr	Asn	Gly	Ser	Ser	Leu	Leu	Ser	Ser	Ser	Asp	Arg	Glu	Leu	Trp	Gln	
234			575					580					585				
236	agg	aaa	cag	gaa	gga	aca	gcg	acc	ctg	tat	gac	agt	ccc	aag	gac	cag	1888
237	Arg	Lys	Gln	Glu	Gly	Thr	Ala	Thr	Leu	Tyr	Asp	Ser	Pro	Lys	Asp	Gln	
238		590					595					600					
240	cat	ttg	aat	gga	agt	gtt	cag	ggt	atc	caa	ggg	cag	act	gaa	act	gaa	1936
241	His	Leu	Asn	Gly	Ser	Val	Gln	Gly	Ile	Gln	Gly	Gln	Thr	Glu	Thr	Glu	
242	605				610					615					620		
244	aac	aca	gaa	act	gtg	gat	agt	gga	atg	agt	aat	ggc	atg	gtg	tgt	gca	1984
245	Asn	Thr	Glu	Thr	Val	Asp	Ser	Gly	Met	Ser	Asn	Gly	Met	Val	Cys	Ala	
246				625						630					635		
248	tct	gga	gac	cgg	agt	cat	tac	agt	gat	tct	cag	ctc	tct	tta	cat	gag	2032
249	Ser	Gly	Asp	Arg	Ser	His	Tyr	Ser	Asp	Ser	Gln	Leu	Ser	Leu	His	Glu	
250				640						645					650		
252	gat	ctt	tct	cca	tgg	aag	gaa	tgg	aat	caa	gga	gct	gat	tta	ggc	ttg	2080
253	Asp	Leu	Ser	Pro	Trp	Lys	Glu	Trp	Asn	Gln	Gly	Ala	Asp	Leu	Gly	Leu	
254			655							660					665		
256	gat	tca	tcc	acc	cag	gaa	ggt	ttt	gat	tat	gaa	aca	aac	agt	ctt	ttt	2128
257	Asp	Ser	Ser	Thr	Gln	Glu	Gly	Phe	Asp	Tyr	Glu	Thr	Asn	Ser	Leu	Phe	
258		670					675						680				
260	gac	caa	cag	ctt	gat	gtt	tac	aat	aaa	gac	cta	gaa	tac	ttg	gga	aag	2176
261	Asp	Gln	Gln	Leu	Asp	Val	Tyr	Asn	Lys	Asp	Leu	Glu	Tyr	Leu	Gly	Lys	
262	685				690						695				700		
264	tgc	cac	agt	gat	ctt	caa	gat	gac	tca	gag	agc	tac	gac	tta	act	caa	2224

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269 Asp Asp Asn Ser Ser Pro Cys Pro Gly Leu Asp Asn Glu Pro Gln Gly
270          720          725          730
272 cag tgg gtt ggc caa tat gat tct tat cag gga gct aat tct aat gag      2320
273 Gln Trp Val Gly Gln Tyr Asp Ser Tyr Gln Gly Ala Asn Ser Asn Glu
274          735          740          745
276 cta tac caa aat caa aac cag ttg tcc atg atg tat cga agt caa agt      2368
277 Leu Tyr Gln Asn Gln Asn Gln Leu Ser Met Met Tyr Arg Ser Gln Ser
278          750          755          760
280 gaa ttg caa agt gat gat tca gag gat gcc cca ccc aaa tca tgg cat      2416
281 Glu Leu Gln Ser Asp Asp Ser Glu Asp Ala Pro Pro Lys Ser Trp His
282 765          770          775          780
284 agt cga tta agc att gac ctt tct gat aag act ttc agc ttc cca aaa      2464
285 Ser Arg Leu Ser Ile Asp Leu Ser Asp Lys Thr Phe Ser Phe Pro Lys
286          785          790          795
288 ttt gga tct aca ctg cag agg gct aaa tca gcc ttg gaa gta gta tgg      2512
289 Phe Gly Ser Thr Leu Gln Arg Ala Lys Ser Ala Leu Glu Val Val Trp
290          800          805          810
292 aac aaa agc aca cag agt ctg agt ggg tat gag gac agt ggc tct tca      2560
293 Asn Lys Ser Thr Gln Ser Leu Ser Gly Tyr Glu Asp Ser Gly Ser Ser
294          815          820          825
296 tta atg ggg aga ttt cgg aca tta tct caa tca act gca aat gag tca      2608
297 Leu Met Gly Arg Phe Arg Thr Leu Ser Gln Ser Thr Ala Asn Glu Ser
298          830          835          840
300 agt acc aca ctt gac tct gat gtc tac acg gag ccc tat tac tat aaa      2656
301 Ser Thr Thr Leu Asp Ser Asp Val Tyr Thr Glu Pro Tyr Tyr Tyr Lys
302 845          850          855          860
304 gca gag gat gag gaa gat tat act gaa cca gtg gct gac aat gaa aca      2704
305 Ala Glu Asp Glu Glu Asp Tyr Thr Glu Pro Val Ala Asp Asn Glu Thr
306          865          870          875
308 gat tat gtt gaa gtc atg gaa caa gtc ctt gct aaa cta gaa aac agg      2752
309 Asp Tyr Val Glu Val Met Glu Gln Val Leu Ala Lys Leu Glu Asn Arg
310          880          885          890
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316 tca tat gaa aca cct tat gaa acc cca caa gat gag ggt tat gat ggt      2848
317 Ser Tyr Glu Thr Pro Tyr Glu Thr Pro Gln Asp Glu Gly Tyr Asp Gly
318          910          915          920
320 cca gca gat gat atg gtt agt gaa gag ggg tta gaa ccc tta aat gaa      2896
321 Pro Ala Asp Asp Met Val Ser Glu Glu Gly Leu Glu Pro Leu Asn Glu
322 925          930          935          940
324 aca tca gct gag atg gaa ata aga gaa gat gaa aac caa aac att cct      2944
325 Thr Ser Ala Glu Met Glu Ile Arg Glu Asp Glu Asn Gln Asn Ile Pro
326          945          950          955
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VERIFICATION SUMMARY

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